Remarks

No new matter has been added. The specification has been amended to direct the entry of this sequence listing after the claims of the above identified application and to provide the SEQ ID NO's next to the specific sequence.

In accordance with 37 C.F.R. § 1.821(g), this submission includes no new matter.

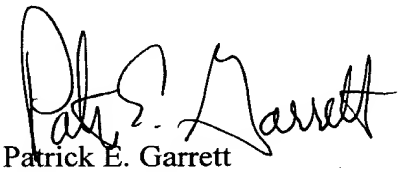
In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above application are the same.

Applicants respectfully request that the Sequence Listing submitted herewith be introduced into the captioned application.

It is respectfully believed that this application is now in condition for examination. Early notice to this effect is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Patrick E. Garrett
Attorney for Applicants
Registration No. 39,987

Date: 1/30/02

1100 New York Avenue, N.W.
Suite 600
Washington, D.C. 20005-3934
(202) 371-2600

Version of Amendment With Markings to Show Changes Made

In the Specification:

The paragraph starting on page 70, line 4, and ending on page 70, line 15:

> Using the computer controlled process DirectedDiversity® (see U.S. Patent 5,463,564), scientists at 3-Dimensional Pharmaceuticals, Inc. have generated a combinatorial library of compounds directed at the active site of human α-thrombin. Approximately 400 compounds were synthesized and assayed by a conventional spectrophotometric kinetic assay in which succinyl-Ala-Ala-Pro-Arg-p-nitroanilide (SEQ ID NO: 1) (Bachem, King of Prussia, PA) served as substrate. Five of these compounds, which are characterized by K_i's that span almost four orders of magnitude in binding affinity, were used to test the range and limits of detection of the thermal shift assay. These five proprietary compounds are listed in Table 3, along with the K_i for each respective compound, as measured by the kinetic assay (last column). K_i's for these compounds ranged from 7.7 nM for 3dp-4026 to 20.0 μM for 3dp-3811.

The paragraph starting on page 19, line 1, and ending on page 19, line 2:

> **Figure 27** is a schematic diagram of a method of screening biochemical conditions that optimize protein folding. This method employs denatured protein tagged with H-H-H-H-H-H (SEQ ID NO: 2) or R-R-R-R-R-R (SEQ ID NO: 3).

The Sequence Listing is added at the end of the application.